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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Sep 13 18:24:01 EDT 2007

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Application No: 10580813 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-09-04 13:46:13.598
Finished: 2007-09-04 13:46:14.532
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 934 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (3)
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W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)

SEQUENCE LISTING

<110> Max Planck Gesellschaft zur Foerderung der Wissensc

<120> Substance binding human IgG Fc receptor IIb (Fc gamma
RIIb)

<130> 30287P_WO HC

<140> 10580813

<141> 2007-09-04

<150> PCT/EP2004/013450

<151> 2004-11-26

<150> EP03027000.3

<151> 2003-11-26

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 172

<212> PRT

<213> human

<220>

<223> Fc gamma RIIa

<400> 1

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1				5					10					15	

Leu	Gln	Glu	Asp	Ser	Val	Thr	Leu	Thr	Cys	Gln	Gly	Ala	Arg	Ser	Pro
			20					25					30		

Glu	Ser	Asp	Ser	Ile	Gln	Trp	Phe	His	Asn	Gly	Asn	Leu	Ile	Pro	Thr
		35					40					45			

His	Thr	Gln	Pro	Ser	Tyr	Arg	Phe	Lys	Ala	Asn	Asn	Asn	Asp	Ser	Gly
	50					55						60			

Glu	Tyr	Thr	Cys	Gln	Thr	Gly	Gln	Thr	Ser	Leu	Ser	Asp	Pro	Val	His
65					70					75					80

Leu	Thr	Val	Leu	Ser	Glu	Trp	Leu	Val	Leu	Gln	Thr	Pro	His	Leu	Glu
				85					90					95	

Phe	Gln	Glu	Gly	Glu	Thr	Ile	Met	Leu	Arg	Cys	His	Ser	Trp	Lys	Asp
			100					105						110	

Lys	Pro	Leu	Val	Lys	Val	Thr	Phe	Phe	Gln	Asn	Gly	Lys	Ser	Gln	Lys
		115					120					125			

Phe	Ser	Arg	Leu	Asp	Pro	Thr	Phe	Ser	Ile	Pro	Gln	Ala	Asn	His	Ser
		130				135						140			

<213> human

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
165 170

<210> 2
<211> 172
<212> PRT
<213> human

<220>
<223> Fc gamma RIIb

<400> 2
Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val
1 5 10 15

Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys
115 120 125

Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Tyr
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro
165 170

<210> 3
<211> 13
<212> PRT
<213> human

<220>
<223> glycopeptide CDE [126-137]

<400> 3
Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Gly
1 5 10

<210> 4
<211> 312
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(312)
<223> variable light region of mAb GB3

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 4
aga att cag ctg acc cag tct cca tcc tcc tta tct gcc tct ctg gga 48
Arg Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

gaa aga gtc agt ctc act tgt cgg gca agt cag gaa att agt ggt tac 96
Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Glu Ile Ser Gly Tyr
20 25 30

tta agc tgg ctt cag cag aaa cca gat gga act att aaa cgc ctg atc 144
Leu Ser Trp Leu Gln Gln Lys Pro Asp Gly Thr Ile Lys Arg Leu Ile
35 40 45

tac gcc aca tcc gct tta gat tct ggt gtc cca aaa agg ttc agt ggc 192
Tyr Ala Thr Ser Ala Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
50 55 60

agt ggg tct ggg tca aat tat tct ctc acc atc agc agc ctt gag tct 240
Ser Gly Ser Gly Ser Asn Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
65 70 75 80

gaa gat ttt gca gac tat tac tgt cta caa tat gct aat tat ccg tac 288
Glu Asp Phe Ala Asp Tyr Tyr Cys Leu Gln Tyr Ala Asn Tyr Pro Tyr
85 90 95

acg ttc gga ggg ggg acc aag ctg 312
Thr Phe Gly Gly Gly Thr Lys Leu
100

<210> 5
<211> 104
<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 5

Arg	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Gly
1				5				10						15	

Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Glu	Ile	Ser	Gly	Tyr
			20					25						30	

Leu	Ser	Trp	Leu	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Ile	Lys	Arg	Leu	Ile
			35				40					45			

Tyr	Ala	Thr	Ser	Ala	Leu	Asp	Ser	Gly	Val	Pro	Lys	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Ser	Asn	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Ser
65					70					75					80

Glu	Asp	Phe	Ala	Asp	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala	Asn	Tyr	Pro	Tyr
				85					90						95

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
							100

<210> 6

<211> 312

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(312)

<223> variable heavy region of mAb GB3

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 6

gtg	cag	ctg	cag	cag	tct	gga	cct	gag	ctg	gtg	aag	cct	ggg	gct	tca	48
Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
1				5				10						15		

gtg	aag	att	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	act	gac	tac	tat	96
Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Tyr	
			20					25					30			

ata	tac	tgg	gtg	aaa	cag	tgg	cct	gga	cag	gga	ctt	gag	tgg	att	gga	144
Ile	Tyr	Trp	Val	Lys	Gln	Trp	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
			35				40					45				

tgg att ttt cct gga act ggt aat act tac tac aat gaa aac ttc aag 192
Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

gac aag gcc aca ctt act ata gat aga tcc tcc agc aca gcc tac atg 240
Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65 70 75 80

ttg ctc ggc agc ctg acc tct gag gac tct gcg gtc tat ttc tgt tat 288
Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95

ggt ccg ttt gct tac tgg ggc caa 312
Gly Pro Phe Ala Tyr Trp Gly Gln
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<210> 7
<211> 104
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 7
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr
20 25 30

Ile Tyr Trp Val Lys Gln Trp Pro Gly Gln Gly Leu Glu Trp Ile Gly
35 40 45

Trp Ile Phe Pro Gly Thr Gly Asn Thr Tyr Tyr Asn Glu Asn Phe Lys
50 55 60

Asp Lys Ala Thr Leu Thr Ile Asp Arg Ser Ser Ser Thr Ala Tyr Met
65 70 75 80

Leu Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Tyr
85 90 95

Gly Pro Phe Ala Tyr Trp Gly Gln
100

<210> 8
<211> 309
<212> DNA
<213> Unknown Organism

<220>
<221> CDS

<222> (1)..(309)

<223> variable light region of mAb CE5

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 8

gag	ctc	acc	cag	tct	cca	gcc	tcc	ctt	tct	gcg	tct	gtg	gga	gaa	act	48
Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Ala	Ser	Val	Gly	Glu	Thr	
1				5				10						15		

gtc	acc	atc	aca	tgt	cga	gca	agt	ggg	aat	att	cac	aat	tat	tta	gca	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gly	Asn	Ile	His	Asn	Tyr	Leu	Ala	
			20					25					30			

tgg	tat	cag	cag	aaa	cag	gga	aaa	tct	cct	cag	ctc	ctg	gtc	tat	tat	144
Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Val	Tyr	Tyr	
		35					40					45				

aca	aca	acc	tta	gca	gat	ggg	gtg	cca	tca	agg	ttc	agt	ggc	agt	gga	192
Thr	Thr	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	
		50				55				60						

tca	gga	aca	caa	tat	tct	ctc	aag	atc	aac	agc	ctg	caa	cct	gaa	gat	240
Ser	Gly	Thr	Gln	Tyr	Ser	Leu	Lys	Ile	Asn	Ser	Leu	Gln	Pro	Glu	Asp	
65					70				75					80		

ttt	ggg	agt	tat	tac	tgt	caa	cat	ttt	tgg	agt	act	cct	cgg	acg	ttc	288
Phe	Gly	Ser	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Ser	Thr	Pro	Arg	Thr	Phe	
			85					90						95		

ggg	gga	ggg	acc	aag	ctc	gag										309
Gly	Gly	Gly	Thr	Lys	Leu	Glu										
			100													

<210> 9

<211> 103

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 9

Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser	Ala	Ser	Val	Gly	Glu	Thr
1				5				10						15	

Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gly	Asn	Ile	His	Asn	Tyr	Leu	Ala
			20					25					30		

Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Val	Tyr	Tyr
		35					40					45			

Thr	Thr	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp
65707580

Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Ser Thr Pro Arg Thr Phe
859095

Gly Gly Gly Thr Lys Leu Glu
100

<210> 10
<211> 339
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (3)..(338)
<223> variable heavy region of mAb CE5

<220>
<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 10

tg cag gag tca gga cct ggc ctg gtg gcg ccc tca cag agc ctg tcc47

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser

151015

atc aca tgc acc gtc tca ggg ttc tca tta acc ggc tat ggt gta aac95

Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Gly Tyr Gly Val Asn

202530

tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg ctg gga atg att143

Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Met Ile

354045

tgg ggt gat gga aac aca gac tat aat tca gct ctc aaa tcc aga ctg191

Trp Gly Asp Gly Asn Thr Asp Tyr Asn Ser Ala Leu Lys Ser Arg Leu

505560

agc atc agc aag gac aac tcc aag agc caa gtt ttc tta aaa atg aac239

Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn

657075

agt ctg cac act gat gac aca gcc agg tac tac tgt gcc aga gag aga287

Ser Leu His Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala Arg Glu Arg

80859095

gat tat agg ctt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc335

Asp Tyr Arg Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser

100105110

tca g339

Ser

<210> 11

<211> 112

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: sequence
comprised by an antibody

<400> 11

Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Ala	Pro	Ser	Gln	Ser	Leu	Ser	Ile
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Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Gly	Tyr	Gly	Val	Asn	Trp
			20				25						30		

Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Met	Ile	Trp
	35					40						45			

Gly	Asp	Gly	Asn	Thr	Asp	Tyr	Asn	Ser	Ala	Leu	Lys	Ser	Arg	Leu	Ser
	50					55					60				

Ile	Ser	Lys	Asp	Asn	Ser	Lys	Ser	Gln	Val	Phe	Leu	Lys	Met	Asn	Ser
65				70					75					80	

Leu	His	Thr	Asp	Asp	Thr	Ala	Arg	Tyr	Tyr	Cys	Ala	Arg	Glu	Arg	Asp
			85					90						95	

Tyr	Arg	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
		100					105						110		